nature portfolio

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Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐ A description of all covariates tested
☒	☐ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	Flow-cytometry data were collected on BD LSR Fortessa. Cytokine measurements were performed with a Luminex bead array platform (Life Technologies). Mice were imaged using a Xenogen IVIS Spectrum system (Caliper Life Science).
Data analysis	Flow-cytometry analysis was performed using Flowjo software (Tree Star Inc. version 10.1). Total bioluminescence flux in mice was quantified using Living Image 4.4 (PerkinElmer). The amount of 51Cr released from the labelled target cells was measured on a liquid scintillation counter (MicroBeta trilux, Perkin Elmer).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The main data supporting the findings of this study are available within the Article and its Supplementary Information. Source data for the tumour-growth experiments are provided with this paper. All raw data generated during the study are available from the corresponding authors on reasonable request.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	We selected sample sizes to make the statistical power greater than 0.8.
Data exclusions	No data were excluded from the experiments.
Replication	All experimental findings were reliably reproduced. Data from each figure have been repeated in independent experiments using different donors.
Randomization	Animals were assigned in all experiments to the treatment and control groups using a randomized approach.
Blinding	The investigators were not blinded. Blinding is unnecessary for the type of assays used, as a uniform gating strategy was used for all samples.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	anti-CCR7–FITC clone 150503, Cat. No. 561271 (BD Pharmingen); anti-CD45RO–PE clone UCHL1, Cat. No. 304206, anti-CD8–H7APC clone SK1, Cat. No. 560179 (BD Biosciences); anti-CD4–BV510 clone OKT4, Cat. No. 317444, anti-CD3–BV605 clone OKT3, Cat. No. 317322, anti-CD14–Pacific Blue (PB) clone HCD14, Cat. No. 325616, anti-CD19–PB clone H1B19, Cat. No. 302232 (BioLegend). The anti-CAR19 idiotype for surface expression of CAR19 was provided by Novartis (Basel, Switzerland).
Validation	Validation of each antibody was done under standard information offered by the supplier.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	All cell lines (NALM-6, MOLM14 and HEK293T) were originally obtained from the American Type Culture Collection (ATCC).
Authentication	Cell-line authentication was performed by the University of Arizona Genetics Core, based on criteria established by the International Cell Line Authentication Committee. Short-tandem-repeat profiling revealed that these cell lines were above the 80% match threshold.
Mycoplasma contamination	Cells were tested for mycoplasma using the MycoAlert detection Kit according to the manufacturer's instructions (Lonza).
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	Male and female 6-to-10-week-old NOD-SCID γc−/−(NSG) mice, which lack an adaptive immune system, were obtained from Jackson Laboratories.
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	All experimental protocols were approved by the Institutional Animal Care and Use Committees (IACUC) of the University of Pennsylvania.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Cells were washed with phosphate-buffered saline (PBS), incubated with LIVE/DEAD Fixable Violet (Molecular Probes) for 15 minutes, and resuspended in fluorescence activated cell sorting (FACS) buffer consisting of PBS, 1% BSA, and 5 mM EDTA. Cells were then incubated with antibodies for 1 hour at 4°C.
Instrument	Flow cytometry was performed on BD LSR Fortessa.
Software	Analysis was performed using Flowjo software (Tree Star Inc. version 10.1).
Cell population abundance	The purity of samples after sorting was confirmed by flow cytometry.
Gating strategy	Positively stained cells were differentiated from background using fluorescence-minus-one (FMO) controls.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.